From: Labiosa, Rochelle
To: Cope, Ben
Subject: RE: Mechanistic HABs Modeling
Date: Wednesday, April 04, 2018 1:54:00 PM

I think the below is generally correct, but with some caveats. This is not the case for marine waters, where lifecycle has been used to do taxon-specific modeling (such as with *A. cantanella* in Puget Sound), and in the Great Lakes nutrient/light/temperature preference is being exploited to predict different taxa dominance. EPA is also employing more satellite tools that are cyanobacteria-specific if not species specific, which can be used to develop refined relationships and expand the spatial scope/applicability of models. You may be aware of it, but here is the webpage: https://www.epa.gov/water-research/cyanobacteria-assessment-network-cyan

As Jason notes, much of the modeling to date has been on capturing HABs bloom dynamics, and less re predicting toxin concentrations. There are many models that predict bloom occurrence, if not toxicity. Let me know if you are looking for particular models (lakes/reservoirs? Streams/marine/estuary? All?) re bloom prevalence, and I can get some cites together.

It is still a challenge to capture the variability in toxins using models, but there is some work going on. The most often used predictive models use satellite data/statistical relationships- such as the Great Lake models (NOAA - Stumpf et al.) - which focus on bloom "severity" linked to cyanobacterial counts expected (e.g., https://coastalscience.noaa.gov/research/stressor-impacts-mitigation/hab-forecasts/) and purely statistical models that link toxins to nutrient concentrations and other factors- Lester Yuan's work (see e.g., https://onlinelibrary.wiley.com/doi/abs/10.1111/fwb.12400).

The focus for many researchers now is on using genomics of toxin producers to better inform/decrease variability and build more mechanistic models.

Gobler et al's EPA grant-funded work (I sent you the contact info for that webinar on 4/18 re his work) I believe includes modeling and toxin production:
https://cfpub.epa.gov/ncer_abstracts/index.cfm/fuseaction/display.abstractDetail/abstract/8378/report/0

Let me know if you need more info and I am happy to follow up.

Thanks, Rochelle

Rochelle Labiosa, Ph.D.
Office of Water and Watersheds
US EPA, Region 10
1200 Sixth Avenue, Suite 900, MC: OWW-191
Seattle, WA 98101-3140
Ph: 206.553.1172

From: Cope, Ben
Sent: Tuesday, April 03, 2018 4:36 PM
To: Labiosa, Rochelle <labiosa.rochelle@epa.gov>
Subject: Fw: Mechanistic HABs Modeling

Hey Rochelle -

Take a look at this email and tell me if you think Jason is right about the status of HAB modeling. I would say yes but am interested in your take. Thanks. -BC

From: Gildea, Jason
Sent: Tuesday, April 3, 2018 3:19 PM
To: Wool, Tim; Cope, Ben; Marshalonis, Dino; Shaikh, Taimur; Johnston, JohnM; Rashleigh, Brenda; Simon, Michelle; Whitlock, Steve; Allen, Ashley; Gossel, Arndt
Subject: Mechanistic HABs Modeling

Hey Modelers,

I've gotten myself entangled in the draft HABs criteria that EPA has released (available here: https://www.epa.gov/wqc/draft-human-health-recreational-ambient-water-quality-criteria-andor-swimming-advisories)

Draft Human Health Recreational Ambient Water Quality ...

www.epa.gov

Information related to Draft Human Health Recreational Ambient Water Quality Criteria and/or Swimming Advisories for Microcystins and Cylindrospermopsin

I've been asked a specific question – Can we (and have we) modeled cyanotoxins using any of the mechanistic surface water quality models? And in particular, for TMDL and/or permitting applications?

If you have any input on this, could you please give me a call or reply to this message? Also, it would be great if you could point to any specific TMDLs where this has been done.

It seems that it would be difficult to mechanistically model cyanotoxins, as we don't seem to really understand the linkages between cyanobacteria and the toxins that they sometimes produce.

I think that the modeling answer is this (outlined in my attached figure):

Ve often model nutrients, and can do that pretty well

Ve often model algae and chl-a, and can do that well

Ve sometimes model cyanobacteria, but this can be difficult and data intensive

Ve almost never model specific cyanobacteria species, cause we never have the data and don't fully understand species specific dynamics

Ve never mechanistically model cyanotoxins, because we cannot directly relate cyanobacteria to cyanotoxins. However, we sometimes use empirical approaches combined with mechanistic approaches to get from nutrients to HABs/cyanotoxins

Thanks for your input,

Jason
Jason Gildea
Hydrologist, EPA Region 8
10 West 15th Street, Suite 3200
Helena, MT 59626
(406)457-5028
Gildea.Jason@epa.gov